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> wherein the position of the mutation is determined by counting from the first amino acid of a mature cellobiohydrolase subsequent to deletion of the preceding 17 amino acid signal sequence, and wherein the first 8 amino acids of the mature wild-type cellobiohydrolase are Glutamine, Serine, Alanine, Cysteine, Threonine, Leucine, Glutamine, and Serine.

If the Examiner approves of this approach, Applicants will provide a complete claim set with the proposed amendments.

Add SEQ ID NO: 98 to the sequence listing which would represent the mature protein, 2. i.e. the protein resulting from the removal of the signal sequence from the fusion protein represented by SEQ ID NO: 5. This approach is supported by the sequence listing filed on January 14, 2002 (and May 6, 2003) which had four polypeptide sequences representing the product of site directed mutagenesis of the cbh1 gene. None of the four sequences contain the signal sequence, and they show various combinations of asparagines residues at positions 45, 270, and/or 384 replaced with alanine. Support is also found in Figure 1 which, as discussed above, shows the coding sequence for the fusion protein and distinguishes the signal sequence from the glucoamylase protein.

Applicants believe both approaches address the Examiner's concerns. The third approach of amending the residue numbers in the claims was considered, but like the Examiner, Applicants believe this approach may not make the claims clearer. If the Examiner finds either approach acceptable, Applicants will provide the necessary amended claim sct or revised sequence listing in short order.

Applicants appreciate the courtesy extended by the Examiner in calling both Paul White and Paul Prendergast to discuss his concerns regarding this case. If the Examiner has additional questions or wishes to discuss this case further, please contact Paul Prendergast at the phone number listed below after November 12, 2007.

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Respectfully submitted,

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Date: 1/8/07

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